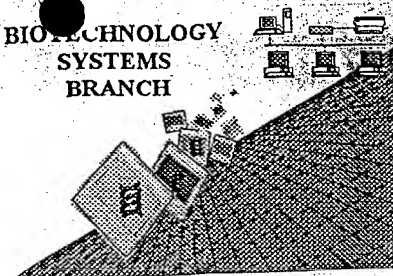




## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIO TECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/761,142  
Source: OIPE  
Date Processed by STIC: 1/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

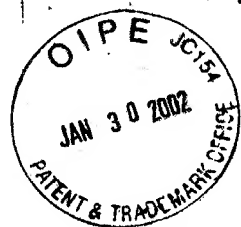
TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**



VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001  
TIME: 11:19:35

Input Set : A:\31133A.ST25.txt  
Output Set: N:\CRF3\01302001\I761142.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1221 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:1221 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
L:1221 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:1221 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
L:1221 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26  
L:1285 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:1285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
L:1285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:1285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
M:340 Repeated in SeqNo=26  
L:1286 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:1286 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
L:1286 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:1286 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
L:1287 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:1287 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26  
L:1287 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:1287 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26  
L:1839 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32  
L:1839 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:32  
L:1839 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:32  
L:1839 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32  
L:1839 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32  
L:11047 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:153  
L:11047 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:153  
L:11047 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:153  
L:11047 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:153  
L:11047 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:153  
L:19618 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:258  
L:19618 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:258  
L:19618 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:258  
L:19618 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:258  
L:19618 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:258  
L:28080 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:356  
L:28080 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:356  
L:28080 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:356  
L:28080 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:356  
L:28080 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:356

09/76/142 6

<210> 26  
 <211> 6413  
 <212> DNA  
 <213> Drosophila melanogaster

&lt;400&gt; 26

```

gaattccttc acaggcggtt tcttgccgc attatcgta atattgtgtg tggacatgta 60
cagctcgcat tgctgcacta ttttatccaa ttttcgaatt tcgctcagtt ccacgcaaga 120
tttgtgggac atttttaagt ctgcaaagta tagaaacgaa aaagtgttgc aaattataat 180
caaacattcg caaagctcag aatatccgga ttcgtaagca aattcaaata aatcttcgct 240
taaaaaaac ttaataataa atccaaaatt tccacttact ccagattgaa attggcgaaa 300
actgcgattt cttacctaat gcactttctt atttacttgc aaatcaaac agaacaggta 360
tgacatgcac gcggagaaat caggagtggg aaatcatttt caatcaatta aaaacacttc 420
aattcgatct tgttcggttac acatactcta ctttttaaat atcatagata aaataaaaaa 480
atgaatagat gtatgtaaat acatggcatt ttcatttcga agtcaactgc tttataagac 540
caactttttt ttcccgggtg aatcaggctt tgcttttctg aaattttcag acatgcgtac 600
tgctttcggt tttcaaagat tcgaaaccac cgtgattttc gaaccattgt tattttcctt 660
ctcgcatctg gtcacactat tttcaaagc aaacaattga tttttcctgc taaacaaaag 720
tggttgaaaa tgcgggaat cgctgccaaa aagattgccg aagcggagga cctggtgaag 780
caggccgaga agaggtatcc ccaacaaaaa tatccttata aaggggtttc caaataacac 840
ccatctttat ttgcagcttg aagttgtcca tgctgaaatg ggttctgat tacgatagt 900
ctgcggatga gtattccaaa gctggtgagt ttcacaaagt aggagtgact aatatcacc 960
agagtatcta tctataaaaa cattgtgaca tcaatgagat atgtaaatac tatgaattac 1020
agctaacgat tatcccaaag tatccataac ttgcaagata cacacatatt ggtgtacaat 1080
tatgtatctt tcttttacct ttttaattgc agccactgca tatcgaatag ctaaaagtta 1140
tgataagagc aaggagtgtt ttctgaaggc aatcgacgcc tataaaaaa acaagtcttg 1200
gttccatgct gcaaaggcat acgaacaggt gagcttaaat tgaagttaat ataagtgaag 1260
ttaataggaa atttaaaccc tctaaatgtg cacatcttct agatcatttt gctgtcaaa 1320
gatgccgata agctacacga agttgaggaa tacgccaca aatcggcgag tttgtatcaa 1380
cagcacggtt cccagaggc agccgcaccc gccctggata aagccgcaa gttactgaa 1440
tccaagcatc ctgacatggc tttgcgcttc tatcagcatg ctctagaagt cataatggtt 1500
cgtcctattt gacactgctc tagtcaattc cattcttaaa ctattaattt tatacttacc 1560
cgacagatcg aggattccgt ccgtcaagca gccgagtatg atcaaaaagt tccaggatac 1620
tggtcaaact aaggaggtat gtacctatga ttgcaacgaa tcactttggg tatccttagc 1680
ttatatcatc caatcactcc aggtacgacg aagccacgaa tgcgctcaa aaggagatca 1740
gcttgaatca gcaaacggaa tcttacggac aaattggacg cctagtgttg gccctgggtg 1800
tggtccaact ggctcgcggt gattccgtgg aagccgaaaa gaccttcagg gagtggggaa 1860
actgctgcga gccagaggaa gtgtccacac tgcagacct tctgcaagcc ttcgatgacg 1920
aggatcccga gttagctgct aggatgctgg catccatt catacgacat atggatgttg 1980
agtacgctat tctatctaaa aacattccac tacctcaggg tatacagatg gagaagaagg 2040
ctggcgacac tgctgctgtg agtattttta ttctaaaaat ggaatttgca atttttgttt 2100

```

(Partial listing of sequence 26 - due to size of sequence, only first error shown - similar errors exist in the rest of the sequence)

→ see  
 item 10 or  
 Error Summary  
 sheet

FYI

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## RAW SEQUENCE LISTING

DATE: 01/30/2001

PATENT APPLICATION: US/09/761,142

TIME: 11:19:34

Input Set : A:\31133A.ST25.txt

Output Set: N:\CRF3\01302001\I761142.raw

```

275 atttaccggg cgttaagacc caccgaatgc ggttaattta agtgataata taatatatta 420
276 aataagaata tgttaatacg tgtaccctgt gacaaatggt tacagtctct aactaattcg 480
277 tactttcgta tttttacaaga acgtaaacgt acgatatacg agtatctaaa agtaaaacca 540
278 cgaatcggtt atgtttacgg tttacggatt acgagtaaaa tggatatcaa tcttttgatc 600
279 aactacctat cgaacctaac agactgaagg tttacattca acttttttac tgcgacatct 660
280 gggattactt agcagcaaca taataaata aaccgtgggg tegtgatgtg cacyttaaat 720
281 aataaatttc acgaacagcg cgttaatttt ataataatcc agtcagtgtt tacatataaa 780
282 tctgaactt cgaacgacta gttgctaaat taticattga aagtggataa tttttattat 840
283 ttgggtttt gataatgcgg aatagccatc cacaatttat tattacgtaa ggtatatcga 900
284 tcaaggactt caagtatcgg tgttggaaac gttcattaaa taattcaata accccgggtg 960
285 gaaatacaaa atcaagatt gagacgctct ttctacaagg aagttcttct ttatctaatc 1020
286 cttcattaaa tcaggtatta aaaggaatca tgattcttga attgattgat aaacaaagg 1080
287 gaaagcaagt ctgcacgttg cacaagaaga agaggacacc gcaatgggtg accccaagcc 1140
288 ggcagagcca gattccgtcg ataccagcc gtgaacgcc tctctgtcaa aagcctcagc 1200
289 ggaaggaccc gtacatgcac cggaaacttc acagcatggt cataaggtat atgcactcat 1260
290 ttgaagcaag tgttgacgtt cagtgtctga ttgaqaaac gtaagtcatg gattaaacgt 1320
291 caccggaaca atatcggcgg gaccgagga tggagaagtg gaagtgcgc tacgccctcg 1380
292 tctgaactcc gtccaagctc ctcccgtaag cgttgagaa gctcgtttc tgggtgtcgc 1440
293 tctgtttcta cgtcgttcac gtgtcggaga agccgaagac gcgtlaactc cctggcgctc 1500
294 tgatgaaat cctcctcgtg ccgcgggacg ggtcgtcgac gacgatgcg aagctgacga 1560
295 ggttcggcgg cgtgcagatg ctctccctca caggttggtt ccgccatcga tgagactctt 1620
296 acgtccgctt cgaattgatg atgtcagctt accgctagta accggagctc cactctgtaa 1680
297 ttgtgtatgc gtccattttt aagtgaacgg tgttcccatg aactcgtgtt cccatacaaa 1740
298 gccgtgcagg gaataccttc tcaataggtt attgaaaact taattgcgtg tgttgactga 1800
299 gtcacttgtt taaaattgat gaaaaaataa gcagtgcgaa tttatcttta gggacggttc 1860
300 tattctacac acaaaaaagt aagtttgta aaacaaatga tttcaaaaga aatttgattt 1920
301 atacagtttc cagctagca atgataata catgtgtcaa caactcgaaa acgaactaca 1980
302 atatttcaat atttcatcat tcttgcaatt ctgtcatttt aaaaaaaat tgtttcaagc 2040
303 gaacagataa gctaaaagcta aggtatagtt ataataaat aatgttaaat acataaaaaag 2100
304 tcaaaaaacc gaacaagtgg cgaatggtta acccgttccg agcgttcata cggttttggt 2160
305 tctatttctt gctcctctgg gggtagttgc tgact 2195
308 <210> SEQ ID NO: 17
309 <211> LENGTH: 227
310 <212> TYPE: PRT
311 <213> ORGANISM: Drosophila melanogaster
313 <400> SEQUENCE: 17
314 Met Glu Lys Ser Phe Pro Ile Thr Pro Trp Lys Tyr Gly Leu Leu Val
315 1 5 10 15
317 Thr Cys Ile Leu Ile Val Thr Cys Asn Val Phe Phe Phe Ser Cys Gly
318 20 25 30
320 Val Thr Thr Trp Gly Ser Ala Val Ser Val Tyr Gly Ser Tyr Gly Ser
321 35 40 45
323 Ala Leu Cys Gly Gly Ala Val Phe Gly Val Ala Phe Leu Gly Met Tyr
324 50 55 60
326 Val Ala Leu Lys Val Ser Tyr Lys Tyr Ser Ile Tyr Tyr Leu Ile Cys
327 65 70 75 80
329 Ser Gly Leu Val Ile Ala Ala Leu Gly Ser Tyr Leu Phe Thr Phe Thr
330 85 90 95
332 Ala Met Arg Glu Gln Leu Met Gly Arg Phe Glu Glu Arg Met Arg Asp

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001  
 TIME: 11:19:34

Input Set : A:\31133A.ST25.txt  
 Output Set: N:\CRF3\01302001\I761142.raw

```

205 acgcggatct gcagcagacc cccgaccacc tctatctgga cgggtgcac gaaaagggtgc 660
206 agagcttcta cgaagcgac aagctgcgct tcatcatagt gtctgggtg ctagtggcct 720
207 tcgagttaat ctgcttcgcc ttggccgtgt ttctggccat tagttttaag aacagcagc 780
208 gacggatgga gttctagttc taggttcggy taatctcgag ctatccaaca gtacaaactc 840
209 ggaatcgggg tctcgtctgt atttttctct tcaacatttc ataaccuaat gcaaaaggaca 900
210 gtcataaatt attcaactct accttaattgt aacctgtaat taaagtacat attgtagtt 960
211 caattaccca ttataagtat cataataaat glgcgcgtgt ttgttttcac atga 1014
214 <210> SEQ ID NO: 15
215 <211> LENGTH: 208
216 <212> TYPE: PRT
217 <213> ORGANISM: Drosophila melanogaster
219 <400> SEQUENCE: 15
220 Met Gly Cys Ala Thr Ser Val Lys Ile Ala Ser Ile Val Leu Asn
221 1 5 10 15
223 Ala Val Leu Gly Phe Leu Ala Ala Gly Ala Ile Gly Trp Ile Ala Tyr
224 20 25 30
226 Asn Ala Asp Thr Glu Thr Glu Glu Phe Val Ile Ala Ala Tyr Ile Ala
227 35 40 45
229 Cys Ser Leu Ile Leu Val Phe Ala Leu Leu Gly Ile Phe Ala Ala Ile
230 50 55 60
232 Arg Glu Ser Val Val Leu Thr Ala Thr Ser Ala Val Phe Leu Leu Ile
233 65 70 75 80
235 Leu Ala Ile Leu Gln Ile Val Ser Thr Cys Leu Phe Leu His Glu Phe
236 85 90 95
238 Asp Val Lys Ser Gly Arg Asp Met Val Glu Val Ala Trp Gln Ala Asn
239 100 105 110
241 Asn Met Asp Ser Leu Gln Gln Lys His Glu Cys Cys Gly Gln Ser Ser
242 115 120 125
244 Ala Gln Asp Tyr Ile His Leu Ser Leu Leu Ile Pro Pro Ser Cys Tyr
245 130 135 140
247 Ala Asp Leu Gln Gln Thr Pro Asp His Leu Tyr Leu Asp Gly Cys Ile
248 145 150 155 160
250 Glu Lys Val Gln Ser Phe Tyr Glu Ser Asp Lys Leu Arg Phe Ile Ile
251 165 170 175
253 Val Ser Trp Val Leu Val Ala Phe Glu Leu Ile Cys Phe Ala Leu Ala
254 180 185 190
256 Val Phe Leu Ala Ile Ser Phe Lys Asn Lys Gln Arg Arg Met Glu Phe
257 195 200 205
263 <210> SEQ ID NO: 16
264 <211> LENGTH: 2195
265 <212> TYPE: DNA
266 <213> ORGANISM: Drosophila melanogaster
268 <400> SEQUENCE: 16
269 tacctcttca gcaaaagggtt ttgtgggacc ttcattgcgg atgaccagtg gacgtaagag 60
270 taacaccatt cactttttct acgcgtaaag gggtaaggtc tcgaaagggt aaaagggtc 120
271 ggactgggtt tacccttaga acgtgttgtg ggccactacg ctcgttactc ggttttagct 180
272 ttttagttat aacgcgggtt caagtgtaga aagcgtttct tcgtttttta ccactgttac 240
273 tcggcgattt ctgatatttg tttagctacg ttagagtttt ttataaatat ttacgtatta 300
274 tggacaagtg tatgaatgta ttaaggcggo cgttcgacaa acattaaaaa cyttatagat 360

```

RAW SEQUENCE LISTING                      DATE: 01/30/2001  
 PATENT APPLICATION: US/09/761,142        TIME: 11:19:34

Input Set : A:\31133A.ST25.txt  
 Output Set: N:\CRF3\01302001\I761142.raw

```

139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial Sequence
142 <220> FEATURE:
143 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
144     Sequence Sp3
146 <400> SEQUENCE: 10
147 gaqtaagcaa agctttaact atgt                24
150 <210> SEQ ID NO: 11
151 <211> LENGTH: 23
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
157     Sequence Sp6
159 <400> SEQUENCE: 11
160 tgaccacatc caaacatcct ott                23
163 <210> SEQ ID NO: 12
164 <211> LENGTH: 25
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
170     Sequence Sp5
172 <400> SEQUENCE: 12
173 qcatcacaaa aatcgacgt caagt                25
176 <210> SEQ ID NO: 13
177 <211> LENGTH: 19
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
183     Sequence SpeI
185 <400> SEQUENCE: 13
186 gacactcaga atactatct                19
189 <210> SEQ ID NO: 14
190 <211> LENGTH: 1014
191 <212> TYPE: DNA
192 <213> ORGANISM: Drosophila melanogaster
194 <400> SEQUENCE: 14
195 agcgaacgca gaacgcgcca gaccacaaaag ttcagattcg agagcggata tccgggcgag 60
196 cgttcacgga aatatatttg ttgtttatct gagtccagca acgaalattt aaataaacaa 120
197 aaaacgaact ttattcgtgt gggagagag agtcacaaa atccaataaa atgggttgcg 180
198 ccacgaccag cgtgaagatc gctccatcg ttctgaatgc cgttttaggg ttctttgctg 240
199 ctggggccat cggctggata gcttacaatg cggacacgga gacggaggaa ttctgaatag 300
200 ccgcttacat cgcgtgctcg ctcatcctgg tctttgctct gctgggcata ttccgggcca 360
201 tccgggaatc ggtggtgctg actgcaacga gtgctgtctt cctgctgata ttggccatcc 420
202 tgcagatcgt gagcacctgc ctgttctctc acgagttcga cgtgaagagc ggccgggaca 480
203 tggtyggagt ggcctggcag gcgaacaaca tggattcctt gcagcagaag cagcagtgct 540
204 gcgccagag cagcgccag gactatatcc acctcagcct gctgatcccg cccagctgct 600

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/761,142

DATE: 01/10/2001  
 TIME: 11:19:34

Input Set : A:\31133A.ST25.txt  
 Output Set: N:\CRF3\01302001\I761142.raw

```

68 <400> SEQUENCE: 4
69 ccttagcatg tccgtggggt ttgaat
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 28
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
79     Sequence Pry2
81 <400> SEQUENCE: 5
82 cttgccgacg ggaccacctt atgttatt
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 19
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
92     Sequence Plw3-1
94 <400> SEQUENCE: 6
95 tgtcggcgtc atcaactcc
98 <210> SEQ ID NO: 7
99 <211> LENGTH: 29
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
105     Sequence Pwht1
107 <400> SEQUENCE: 7
108 gtaacgctaa tcactccgaa caggtcaca
111 <210> SEQ ID NO: 8
112 <211> LENGTH: 25
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
118     Sequence Splac2
120 <400> SEQUENCE: 8
121 gaattcaactg gccgtcggtt tacaa
124 <210> SEQ ID NO: 9
125 <211> LENGTH: 22
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
131     Sequence Spl
133 <400> SEQUENCE: 9
134 acacaacctt tcctctcaac aa
137 <210> SEQ ID NO: 10
138 <211> LENGTH: 24

```

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/761,142

DATE: 01/30/2001  
 TIME: 11:19:34

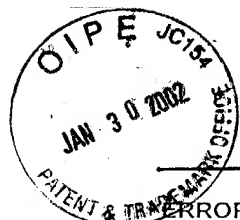
Input Set : A:\31133A.ST25.txt  
 Output Set: N:\CRF3\01302001\I761142.raw

Does Not Comply  
 Corrected Diskette Needed

P.6

OK  
 3 <110> APPLICANT: Kamdar, Kim  
 4 Broadus, Julie  
 5 Stam, Lynn  
 6 Bachmann, Jane  
 8 <120> TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE  
 9 PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF  
 11 <130> FILE REFERENCE: PB/5-31133A  
 13 <140> CURRENT APPLICATION NUMBER: US/09/761,142  
 13 <141> CURRENT FILING DATE: 2001-01-16  
 13 <150> PRIOR APPLICATION NUMBER: US 60/176,418  
 14 <151> PRIOR FILING DATE: 2000-01-14  
 16 <160> NUMBER OF SEQ ID NOS: 361  
 18 <170> SOFTWARE: PatentIn Ver. 2.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 27  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Artificial Sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
 27 Sequence Plac4  
 29 <400> SEQUENCE: 1  
 30 actgtgcgtt aggtcctggt cattggt 27  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 24  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Artificial Sequence  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
 40 Sequence Plac1  
 42 <400> SEQUENCE: 2  
 43 caccacaaggtc tctgctccca caat 24  
 46 <210> SEQ ID NO: 3  
 47 <211> LENGTH: 23  
 48 <212> TYPE: DNA  
 49 <213> ORGANISM: Artificial Sequence  
 51 <220> FEATURE:  
 52 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
 53 Sequence Pry4  
 55 <400> SEQUENCE: 3  
 56 caatcatatc gctgtctcac tca 23  
 59 <210> SEQ ID NO: 4  
 60 <211> LENGTH: 26  
 61 <212> TYPE: DNA  
 62 <213> ORGANISM: Artificial Sequence  
 64 <220> FEATURE:  
 65 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
 66 Sequence Pry1





## Raw Sequence Listing Error Summary

**ERROR DETECTED SUGGESTED CORRECTION**

SERIAL NUMBER:

09/76/142

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.